

Access DB# 134501

**SEARCH REQUEST FORM**  
Scientific and Technical Information Center

Requester's Full Name: TANE ZARA Examiner #: 77512 Date: 11-30-07  
Art Unit: 1635 Phone Number 301-20765 Serial Number: 07/803,165  
Mail Box and Bldg/Room Location: 2728 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Mutant B types  
Inventors (please provide full names): Sobel et al.

Earliest Priority Filing Date: 3-9-01

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search Seq ID No: 34.  
AA-774

AA data boxes only. me

No size limits

Please search for Interferon  
+ regular data  
boxes.

Thanks

**STAFF USE ONLY**

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>12/1/07</u>	Bibliographic _____	Dr Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>82p</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____



Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MIPDTDYITKDGKRIIRIFKKEKNGEFKIELDPHPQPIYALIKDSDAIDEIKAIKGRERG 60
Db 1 MIPDTDYITKDGKRIIRIFKKEKNGEFKIELDPHPQPIYALIKDSDAIDEIKAIKGRERG 60
Qy 61 KIVRVDAVKVKKKFLGRDVEVWKILFEHPDVPALRGKIRHPAVIDIYEDIPPAKRY 120
Db 61 KIVRVDAVKVKKKFLGRDVEVWKILFEHPDVPALRGKIRHPAVIDIYEDIPPAKRY 120
Qy 121 LIDKGLPMEGDEELKMAFDIETFYHGDGFGKEIIMSYADEBARAVITWKNDLPY 180
Db 121 LIDKGLPMEGDEELKMAFDIETFYHGDGFGKEIIMSYADEBARAVITWKNDLPY 180
Qy 181 VDVVSNREMIKRFVQIVREKDPVLLITYNGDNFDLPYLKRAEKLGVTLILGRDKERPE 240
Db 181 VDVVSNREMIKRFVQIVREKDPVLLITYNGDNFDLPYLKRAEKLGVTLILGRDKERPE 240
Qy 241 PKIHRMGDSFAVEIKGRIFHFDLPFVVRRTINLPYTLAAYEAVLGKTKSLGAEIAMI 300
Db 241 PKIHRMGDSFAVEIKGRIFHFDLPFVVRRTINLPYTLAAYEAVLGKTKSLGAEIAMI 300
Qy 301 WETESMKKLAQYSMEDARATYELGKEFPMEAEALAKLIGOSVWDSRSSTGNLVEMVYL 360
Db 301 WETESMKKLAQYSMEDARATYELGKEFPMEAEALAKLIGOSVWDSRSSTGNLVEMVYL 360
Qy 361 RYAEHNEIAPNKPDEEYRRLRTTYLGGYVKEPBERGLMENITYLDFRCIYPSIIVTN 420
Db 361 RYAEHNEIAPNKPDEEYRRLRTTYLGGYVKEPBERGLMENITYLDFRCIYPSIIVTN 420
Qy 421 VSPDTLEREGCKNYDVAPIVGYKFCDFPGPIPSILGELITMRQELKKMKATIDPIEKK 480
Db 421 VSPDTLEREGCKNYDVAPIVGYKFCDFPGPIPSILGELITMRQELKKMKATIDPIEKK 480
Qy 481 MLDYRQRAVKLANSYGYMGYPKARWYSKCAESVTAWGRHYIEMTIKEIEBEGFKVL 540
Db 481 MLDYRQRAVKLANSYGYMGYPKARWYSKCAESVTAWGRHYIEMTIKEIEBEGFKVL 540
Qy 541 YADTDGFYATIPGKEPRTIKKAKAEFLKYINSLPGLLEEGSYLGRGFVAKRYAVI 600
Db 541 YADTDGFYATIPGKEPRTIKKAKAEFLKYINSLPGLLEEGSYLGRGFVAKRYAVI 600
Qy 601 DSEGRITTRGLEVRPMSEIAKETOAKVLEAILKESVEKAVEIVDVEBEIAKYQVPL 660
Db 601 DSEGRITTRGLEVRPMSEIAKETOAKVLEAILKESVEKAVEIVDVEBEIAKYQVPL 660
Qy 661 EKLVIHQITKDLSEYKALGPHVAIAKRLAKGIVRPGIISYIVLRSGKISDRVYL 720
Db 661 EKLVIHQITKDLSEYKALGPHVAIAKRLAKGIVRPGIISYIVLRSGKISDRVYL 720
Qy 721 SEYPPKHKYDPDYIENQVLPAYLRLIEAFGRKEDOLKQSSQVGLDMLKK 774
Db 721 SEYPPKHKYDPDYIENQVLPAYLRLIEAFGRKEDOLKQSSQVGLDMLKK 774

```

RESULT 2  
AAW29323  
ID AAW29323 standard; protein: 774 AA.

AAW29323;  
20-APR-1998 (first entry)  
XX DNA polymerase with 3'-5' exonuclease activity.  
XX TY Exon: DSM 10597; thermostable; DNA polymerase; 3'-5' exonuclease;  
XX amplification.  
XX Thermococcus sp.  
XX DE19611759-A1.  
XX PD 02-OCT-1997.

XX 25-MAR-1996; 96DE-01011759.  
XX 25-MAR-1996; 96DE-01011759.  
XX (BOEP) BOEHRINGER MANNHEIM GMBH.  
XX Frey B, Niehaus F, Antmanikien G,  
XX MPI; 1997-481494/45.  
XX N-PSDB; AAT86434.  
XX Thermostable DNA polymerase from Thermococcus sp. TY - useful for nucleic  
XX acid amplification.  
XX Claim 1; Page 9-10; 32pp; German.  
XX The present sequence (TY Exon) is a Thermococcus sp. TY (DSM 10597)  
XX thermostable DNA polymerase with 3'-5' exonuclease activity. The enzyme  
XX can specifically amplify nucleic acid fragments of up to 5 kb in high  
XX yields, has an activity half-life of 20 minutes at 90 degrees C, has an  
XX optimum temperature of 70-80 degrees C, has an optimum pH of 7.5,  
XX exhibits optimum activity at a KCl concentration of 80-100 mM, is  
XX magnesium ion-dependent and is inhibited by manganese ions  
SQ Sequence 774 AA;

Query Match 99.1%; Score 3990; DB 2; Length 774;  
Best Local Similarity 99.4%; Pred. No. 2 7e-302; Indels 0; Gaps 0;  
Matches 769; Conservative 1; Mismatches 4;

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Qy 1 MIPDTDYITKDGKRIIRIFKKEKNGEFKIELDPHPQPIYALIKDSDAIDEIKAIKGRERG 60
Db 1 MIPDTDYITKDGKRIIRIFKKEKNGEFKIELDPHPQPIYALIKDSDAIDEIKAIKGRERG 60
Qy 61 KIVRVDAVKVKKKFLGRDVEVWKILFEHPDVPALRGKIRHPAVIDIYEDIPPAKRY 120
Db 61 KIVRVDAVKVKKKFLGRDVEVWKILFEHPDVPALRGKIRHPAVIDIYEDIPPAKRY 120
Qy 121 LIDKGLPMEGDEELKMAFDIETFYHGDGFGKEIIMSYADEBARAVITWKNDLPY 180
Db 121 LIDKGLPMEGDEELKMAFDIETFYHGDGFGKEIIMSYADEBARAVITWKNDLPY 180
Qy 181 VDVVSNREMIKRFVQIVREKDPVLLITYNGDNFDLPYLKRAEKLGVTLILGRDKERPE 240
Db 181 VDVVSNREMIKRFVQIVREKDPVLLITYNGDNFDLPYLKRAEKLGVTLILGRDKERPE 240
Qy 241 PKIHRMGDSFAVEIKGRIFHFDLPFVVRRTINLPYTLAAYEAVLGKTKSLGAEIAMI 300
Db 241 PKIHRMGDSFAVEIKGRIFHFDLPFVVRRTINLPYTLAAYEAVLGKTKSLGAEIAMI 300
Qy 301 WETESMKKLAQYSMEDARATYELGKEFPMEAEALAKLIGOSVWDSRSSTGNLVEMVYL 360
Db 301 WETESMKKLAQYSMEDARATYELGKEFPMEAEALAKLIGOSVWDSRSSTGNLVEMVYL 360
Qy 361 RYAEHNEIAPNKPDEEYRRLRTTYLGGYVKEPBERGLMENITYLDFRCIYPSIIVTN 420
Db 361 RYAEHNEIAPNKPDEEYRRLRTTYLGGYVKEPBERGLMENITYLDFRCIYPSIIVTN 420
Qy 421 VSPDTLEREGCKNYDVAPIVGYKFCDFPGPIPSILGELITMRQELKKMKATIDPIEKK 480
Db 421 VSPDTLEREGCKNYDVAPIVGYKFCDFPGPIPSILGELITMRQELKKMKATIDPIEKK 480
Qy 481 MLDYRQRAVKLANSYGYMGYPKARWYSKCAESVTAWGRHYIEMTIKEIEBEGFKVL 540
Db 481 MLDYRQRAVKLANSYGYMGYPKARWYSKCAESVTAWGRHYIEMTIKEIEBEGFKVL 540
Qy 541 YADTDGFYATIPGKEPRTIKKAKAEFLKYINSLPGLLEEGSYLGRGFVAKRYAVI 600
Db 541 YADTDGFYATIPGKEPRTIKKAKAEFLKYINSLPGLLEEGSYLGRGFVAKRYAVI 600
Qy 601 DSEGRITTRGLEVRPMSEIAKETOAKVLEAILKESVEKAVEIVDVEBEIAKYQVPL 660
Db 601 DSEGRITTRGLEVRPMSEIAKETOAKVLEAILKESVEKAVEIVDVEBEIAKYQVPL 660

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 1, 2004, 16:24:27 ; Search time 204 Seconds  
(without alignments)  
2183.039 Million cell updates/sec

Title: US-09-803-165-34

Perfect score: 4026

Sequence: 1 MIFEDYITKDGKPIIRIFK.....KEDLYQSSKQVGLDPAWLKK 774

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1325181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	3446.5	85.6	1829 1 DPOL_THER1	033845 thermococcus
2	3356	83.4	1702 1 DPOL_THER1	P30317 thermococcus
3	3253.5	80.8	773 1 DPOL_THER1	P56689 thermococcus
4	3212	79.8	775 2 Q9P9K4	Q9P9K4 pyrococcus
5	3211	79.6	775 2 Q9H9R6	Q9H9R6 pyrococcus
6	3204.5	79.6	775 1 DPOL_THER9	Q56366 thermococcus
7	3164.5	78.6	771 1 DPOL_PYRAB	P77918 pyrococcus
8	3151	78.3	775 1 DPOL_PYRAB	P61876 pyrococcus
9	3151	78.3	775 1 DPOL_PYRAB	P61876 pyrococcus
10	3141.5	78.0	773 2 Q7S1G7	Q7S1G7 desulfurococcus
11	3081	76.5	759 2 Q9H9R8	Q9H9R8 pyrococcus
12	2934.5	72.9	1312 1 DPOL_PYRSD	Q51134 pyrococcus
13	2905	72.2	733 2 Q7S1G8	Q7S1G8 desulfurococcus
14	2886	71.7	1235 1 DPOL_PYRHO	Q59610 pyrococcus
15	2809	69.8	1523 1 DPOL_THERM	P74918 thermococcus
16	2782	69.1	1671 1 DPOL_PYRKO	P77933 pyrococcus
17	2769.5	68.8	1569 1 DPOL_THER8	Q9H884 thermococcus
18	2635.5	63.0	1668 1 DPOL_THERY	Q9H805 thermococcus
19	1549.5	38.5	784 2 Q6M051	Q6M051 methanococcus
20	1549.5	38.5	784 2 Q6M051	Q6M051 methanococcus
21	1392.5	34.6	830 2 Q8T9W5	Q8T9W5 methanopyrus
22	1392	34.6	824 1 DPOL_METVO	P52025 methanococcus
23	1301	32.3	781 1 DPOL_ARCFU	Q29753 archaeoglobus
24	1292	32.1	1634 1 DPOL_METUA	Q58995 methanococcus
25	1209.5	29.9	30.0 DPOL_METHH	Q27276 methanobacterium
26	1204.5	29.9	781 2 Q9P9N1	Q9P9N1 sulfatobacterium
27	1204.5	29.9	781 2 Q9P9N1	Q9P9N1 sulfatobacterium
28	1190	28.6	785 2 Q8ZVW2	Q8ZVW2 pyrobaculum
29	1149.5	28.3	784 1 DPOL_ASRPE	Q93746 aeropyrum
30	1138	28.3	784 1 DPOL_ASRPE	Q93746 aeropyrum
31	1125	27.9	785 2 Q9P9M2	Q9P9M2 pyrobaculum

32	914	22.7	933 2 Q8PVG1	Q8PVG1 methanobacterium
33	913	22.7	937 2 Q8T8B3	Q8T8B3 methanobacterium
34	821	20.4	676 2 Q7AN74	Q7AN74 nanorarchaeum
35	821	20.4	676 2 ARK38923	ARK38923 nanorarchaeum
36	774	19.2	195 2 Q9H85	Q9H85 thermococcus
37	711	17.7	974 2 Q6S0P5	Q6S0P5 encephalito
38	697.5	17.3	1105 1 DPOL_ORYSA	Q91866 oryza sativa
39	693.5	17.2	1088 1 DPOL_SOYBN	Q48901 glycine max
40	691.5	17.2	1054 2 Q6BH09	Q6BH09 debaromyces
41	691	17.2	763 1 DPOL_SUISO	Q05706 sulfobolus
42	676.5	16.8	764 1 DPOL_ARATH	Q91871 arabidopsis
43	676.5	16.8	1081 1 DPOL_ARATH	Q91871 arabidopsis
44	665.5	16.5	1026 2 Q7YVP5	Q7YVP5 typharostoma
45	657.5	16.3	1038 1 DPOL_CANAL	P46588 candida alb

## ALIGNMENTS

```

RESULT 1
DPOL_THER1
ID DPOL_THER1 STANDARD: PRT, 1829 AA.
AC Q33845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 05-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN Name=pol;
OS Thermococcus sp. (strain TV).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=110163;
RN [1]
RP SOURCE FROM N.A.
RS MEDLINE=96094267; PubMed=9434178;
RA Niehaus F., Frey B., Antikamian G.;
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase
RT from the hyperthermophilic archaeon Thermococcus sp. TV.";
RL Gene 204:153-158(1997).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA) (N).
CC -!- PRT: This protein undergoes a protein self splicing that involves
CC a post-translational excision of the three intervening regions
CC (introns) followed by peptide ligation.
CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL, Y13030, CAAT73475.1; -.
CC HSP: P77933, IGCC.
CC InterPro: IPR006172; DNA_pol_B.
CC InterPro: IPR006133; DNA_pol_B_exo.
CC InterPro: IPR006134; DNA_pol_B_exo.
CC InterPro: IPR006142; INTEIN.
CC InterPro: IPR004042; intein_endonuc.
CC InterPro: IPR006141; intein_S.
CC InterPro: IPR004578; pol2.
CC Pfam: PF00136; DNA_pol_B_4.
CC Pfam: PF00136; DNA_pol_B_exo_1.
CC PRINTS: PRO0379; INTEIN.
CC TIGRfam: TIGR01443; intein_Cterm; 3.
CC TIGRfam: TIGR01445; intein_Nterm; 3.
CC TIGRfam: TIGR00592; pol2; 2.
CC PROSITE: PS00116; DNA_POLYMERASE_B; FALSE_NEG.
CC PROSITE: PS00818; INTEIN_C_TERM; 3.
CC PROSITE: PS00819; INTEIN_ENDONUCLEASE; 2.
CC PROSITE: PS00817; INTEIN_N_TERM; 3.

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Db 1 MIDDTDTITDKGPIIRIRIKKENGFEKILDPHPQPIYALTKDSDAIBELIKAIKBERRG 60
QY 61 KIYRVVDVAVKVKKFLGRDVEVWKLIIEFHQDVPALRGKIREHPAVIDIYEYDIPAKKY 120
Db 61 KTVRVDAVAVKVKKFLGREVEVWKLIIEFHQDVPANMGKIREHPAVDIVEYDIPAKKI 120
QY 121 LIDGGLIPMGDEELKMAFDIETFEYHGEDEFGKGIIMISYADEBEARVITKKNIDLPY 180
Db 121 LIDGGLIPMGDEELKMAFDIETFEYHGEDEFGKGIIMISYADEBEARVITKKNIDLPY 180
QY 181 VDVSNEREMIKRFVQIVREKDPVLLITNGDNFDLPYLTKAEKLGVTLLGRDKHPE 240
Db 181 VDVSNEREMIKRFVQIVREKDPVLLITNGDNFDLPYLTKAEKLGVTLLGRDKHPE 240
QY 241 PKIRMGDSFAVELIKGRIHFDLPFVARTINLPYTLAEVYAVLGKTKKLAGABEIAAI 300
Db 241 PKIRMGDSFAVELIKGRIHFDLPFVARTINLPYTLAEVYAVLGKTKKLAGABEIAAI 300
QY 301 WEIYESMKKLAQYSMEDARATYELGKEFFPMEALATLIGOSVADVSRSTGMLVEMYLL 360
Db 301 WEIYESMKKLAQYSMEDARATYELGKEFFPMEALATLIGOSVADVSRSTGMLVEMYLL 360
QY 361 RVAERHBIAPNKEDEBEYRRRLRTTYLGIVKPEPERGLMENTTYLDFRCIYPSIIYTHN 420
Db 361 RVAERHBIAPNKEDEBEYRRRLRTTYLGIVKPEPERGLMENTTYLDFRCIYPSIIYTHN 420
QY 421 VSPPTLEREGCKNDVAVIYVGFCKDPGFIPIIIGELITVNGEIKKKKKAATIDPIEK 480
Db 421 VSPPTLEREGCKNDVAVIYVGFCKDPGFIPIIIGELITVNGEIKKKKKAATIDPIEK 480
QY 481 MLDYROBAVKLHA----- 493
Db 481 MLDYROBAVKLHA----- 493
QY 494 ----- 493
Db 494 ----- 493
QY 541 VNNLFASFENKKIKESYVKYKVALIRHKYKGAVEIQSSGRKINITAGHSLFTVRNGEI 600
Db 541 VNNLFASFENKKIKESYVKYKVALIRHKYKGAVEIQSSGRKINITAGHSLFTVRNGEI 600
QY 494 ----- 493
Db 494 ----- 493
QY 601 KEVSGDGIKESDILVAPKKIKLNEKGVISINIPILISDSEBEYADIVMTISAKGRKAPFK 660
Db 601 KEVSGDGIKESDILVAPKKIKLNEKGVISINIPILISDSEBEYADIVMTISAKGRKAPFK 660
QY 494 ----- 493
Db 661 GMLRTLRMPGBENRIRITFNRVLFLEKGLIKLIPRGYVTDWELKTKYKQLYEKLAG 720
QY 494 ----- 493
Db 721 SVKYNKGRKRYLVFNELIKDISYFPQKELEBWKIGTLNGFRINCILKVDDEGKLLGYV 780
QY 494 ----- 493
Db 781 VSEGYAGQKNNKTGSIYSVTLNEDPVLVLESMQVAKKFKGVAVDRNCVISIKQAVYL 840
QY 494 ----- 493
Db 841 WKCLCGALAKENKRIIPSVILTSPEPVMFLAEVFTGDDIHFPSKREFLSTKSELLANOL 900
QY 494 ----- 493
Db 901 VFLNLSIGISSVKIGFDSGVRYVINEDLPQPTSRKEMTYYSXULIPKELIADVFGKRFQ 960
QY 494 ----- 493
Db 961 KNNTFKKFKELVDSGLNREKAKLLEFFINGDILDRYKSVKEXDYEYGYVYDLSVEDNEN 1020
QY 494 ----- 542
Db 1021 FLVNGGLIYAHNSYTGWQPKARVYSKCAESVJAMGRHITMTIRIRIEKRFKFLYA 1080
QY 543 D----- 543

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Db 1081 DSVSGSEIIIRONGKIRFVKIKDLFSKVDSIGEKEYCILEGEVALTLDDGKLWMPKV 1140
QY 544 ----- 543
Db 1141 PYVMGRANKKMFRTIMLNSWYIDVTEHSHLIGYINTSKTKAKKIGRLKEVVPBLGK 1200
QY 544 ----- 543
Db 1201 AVKSLICPNAPLKDNITKTSIAVKEFWELVGLVGDQNGGDSRWABYYLGLSTGDAEE 1260
QY 544 ----- 543
Db 1261 IKOKLEPLKTYGVISNTYPPKNEKDPNIIAKSLVFKPKRHPKDKGRKRIPEFMYELPV 1320
QY 544 ----- 543
Db 1321 TYIEAFRLGLFSADGTVIRKGVPEIRLTINIDAFLEVRKLMVIGISINSIFAETPNR 1380
QY 544 ----- 543
Db 1381 YNGVSTGYTSKHLRIKNNKRFARIGFLIERQKALLEHKSARVAKNTIDGFDLVHYK 1440
QY 544 ----- 1441
Db 1441 KYEBIPYBGVYDIEVESTHRFFANNILVHNTDGFATIPGEKPELIKKEKAEFLMYINS 1500
QY 573 KLPGLLELEFGPYLRGFPVAKKRYAVIDEGRIITRGLEVVRRDMSIETAKETQAKVLEA 632
Db 1501 KLPGLLELEFGPYLRGFPVAKKRYAVIDEGRIITRGLEVVRRDMSIETAKETQAKVLEA 1560
QY 633 ILKEDSVEKAVELVQVVEEIAKYQVPLEKLVIEHOITKDLSEYXAGHPVAIARLAKLA 692
Db 1561 ILKESVEKAVELVQVVEEIAKYQVPLEKLVIEHOITKDLSEYXAGHPVAIARLAKLA 1620
QY 693 GIKVRGTTIISYIVLRGSGKISDRVITLSEYQPKKXNDPVDYIENOVLPALRTILEAG 752
Db 1621 GIKVRGTTIISYIVLRGSGKISDRVITLSEYQPKKXNDPVDYIENOVLPALRTILEAG 1680
QY 753 YRKEDLKYQSKQVGLDAMWKK 774
Db 1681 YRKEDLKYQSKQVGLDAMWKK 1702

RESULT 2
S67920
DNA-directed DNA polymerase (EC 2.7.7.7) - Thermococcus sp.
C:Species: Thermococcus sp.
C:Date: 17-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S67920
R:Southworth, M.S., Kong, H., Kucera, R.B., Ware, J., Jannasch, H.W., Belter, F.B.
Submitted to the EMBL Data Library, January 1996
A:Description: Cloning, expression and modulation of the 3'-5' exonuclease activity of
A:Reference number: S67920
A:Accession: S67920
A:Molecule type: DNA
A:Residues: 1-775 <SOU>
A:Cross-references: UNIPROT:Q56366; GB:U47108; NID:g1197451; PIDN:AAA8769.1; PID:g1197
A:Experimental source: strain 90N-7
C:Superfamily: DNA polymerase
C:Keywords: DNA binding; nucleotidyltransferase

Query Match 79.6%; Score 3204.5; DB 2; Length 775;
Best Local Similarity 76.6%; Pred. No. 9,4e-159;
Matches 592; Conservative 89; Mismatches 89; Indels 3; Gaps 2;

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